

#2

OIKE

## RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/10/024,450

TIME: 19:02:09

Input Set : A:\Lj5101.txt

Output Set: N:\CRF3\01152002\J024450.raw

ENTERED

4 <110> APPLICANT: Huang, Shi  
5 Chadwick, Robert B.  
7 <120> TITLE OF INVENTION: Methods of Detecting and Treating  
8 Microsatellite-Instability Positive Tumors Using RIZ  
11 <130> FILE REFERENCE: P-LJ 5101  
13 <140> CURRENT APPLICATION NUMBER: US/10/024,450  
13 <141> CURRENT FILING DATE: 2001-12-17  
13 <150> PRIOR APPLICATION NUMBER: US 60/256,582  
14 <151> PRIOR FILING DATE: 2000-12-19  
16 <160> NUMBER OF SEQ ID NOS: 15  
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 6171  
22 <212> TYPE: DNA  
23 <213> ORGANISM: Rattus SP.  
25 <220> FEATURE:  
26 <221> NAME/KEY: CDS  
27 <222> LOCATION: (157)...(5274)  
29 <400> SEQUENCE: 1  
30 gccagatgg cggcggcgcg gccgcgggcg ccagggcgac ggcggcggct gaggtctctg 60  
31 gctcgctgaa gcgttggcac gtcgcgctct gggtcatgt aatcaaagaa gtttctttgt 120  
32 tgtgtgtatc ttacagaaac acaacaggaa ttgaaa atg cat cag aac act gag 174  
33 Met His Gln Asn Thr Glu  
34 1 5  
36 tct gtg gca gcc act gag act ctg gct gag gta cct gaa cat gtg ctt 222  
37 Ser Val Ala Ala Thr Glu Thr Leu Ala Glu Val Pro Glu His Val Leu  
38 10 15 20  
40 cga gga ctt cca gag gaa gta aga ctt ttc cca tct gca gtc gac aag 270  
41 Arg Gly Leu Pro Glu Glu Val Arg Leu Phe Pro Ser Ala Val Asp Lys  
42 25 30 35  
44 act cgg att ggt gtc tgg gct act aaa cca att tta aaa ggg aaa aag 318  
45 Thr Arg Ile Gly Val Trp Ala Thr Lys Pro Ile Leu Lys Gly Lys Lys  
46 40 45 50  
48 ttt ggg cca ttt gtt ggt gat aag aag aag aga tcc cag gtt agg aat 366  
49 Phe Gly Pro Phe Val Gly Asp Lys Lys Lys Arg Ser Gln Val Arg Asn  
50 55 60 65 70  
52 aat gtg tac atg tgg gag gtc tac tac cca aat ttg ggg tgg atg tgc 414  
53 Asn Val Tyr Met Trp Glu Val Tyr Tyr Pro Asn Leu Gly Trp Met Cys  
54 75 80 85  
56 att gat gcc acc gat ccg gag aag ggc aac tgg cta cgc tat gtg aac 462  
57 Ile Asp Ala Thr Asp Pro Glu Lys Gly Asn Trp Leu Arg Tyr Val Asn  
58 90 95 100  
60 tgg gct tgc tca gga gaa gag cag aat tta ttt cca ctg gaa atc aac 510  
61 Trp Ala Cys Ser Gly Glu Glu Asn Leu Phe Pro Leu Glu Ile Asn  
62 105 110 115  
64 aga gcc att tac tat aaa acc tta aag cca atc gcg cct ggc gag gag 558  
65 Arg Ala Ile Tyr Tyr Lys Thr Leu Lys Pro Ile Ala Pro Gly Glu Glu

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66	120	125	130	
68	ctc ctg gtc tgg tac aat ggg gaa gac aac cct gag ata gca gct gcg	606		
69	Leu Leu Val Trp Tyr Asn Gly Glu Asp Asn Pro Glu Ile Ala Ala Ala			
70	135 140 145 150			
72	att gag gaa gag cga gcc agc gcc cgg agc aag cgg agc tcc ccg aag	654		
73	Ile Glu Glu Glu Arg Ala Ser Ala Arg Ser Lys Arg Ser Ser Pro Lys			
74	155 160 165			
76	agc cgc aga ggg aag aag aaa tca cac gag aac aaa aac aaa ggc atc	702		
77	Ser Arg Arg Gly Lys Lys Lys Ser His Glu Asn Lys Asn Lys Gly Ile			
78	170 175 180			
80	aga acc cac ccc aca cag ctg aag gca agt gag ctg gac tct acc ttt	750		
81	Arg Thr His Pro Thr Gln Leu Lys Ala Ser Glu Leu Asp Ser Thr Phe			
82	185 190 195			
84	gca aac atg agg ggc tct gca gaa ggt cca aaa gaa gag gat gag agg	798		
85	Ala Asn Met Arg Gly Ser Ala Glu Gly Pro Lys Glu Glu Asp Glu Arg			
86	200 205 210			
88	cct ttg gct tcg gca cct gag cag cca gcc cct ctg ccg gag gtg ggg	846		
89	Pro Leu Ala Ser Ala Pro Glu Gln Pro Ala Pro Leu Pro Glu Val Gly			
90	215 220 225 230			
92	aat caa gat gca gtt cca cag gtg gcc atc cct ctc cct gcc tgc gag	894		
93	Asn Gln Asp Ala Val Pro Gln Val Ala Ile Pro Leu Pro Ala Cys Glu			
94	235 240 245			
96	cca cag cca gag gta gat ggg aaa caa gaa gtc aca gac tgt gag gtc	942		
97	Pro Gln Pro Glu Val Asp Gly Lys Gln Glu Val Thr Asp Cys Glu Val			
98	250 255 260			
100	aat gat gtg gag gaa gag gag ctg gaa gag gaa gag gag ctg gaa gag	990		
101	Asn Asp Val Glu Glu Glu Glu Leu Glu Glu Glu Glu Glu Leu Glu Glu			
102	265 270 275			
104	gag gag gag gag gag ttg gga gaa gat ggg gta gaa gaa gca gac atg	1038		
105	Glu Glu Glu Glu Glu Leu Gly Glu Asp Gly Val Glu Glu Ala Asp Met			
106	280 285 290			
108	ccg aat gaa agc tct gcg aaa gag ccg gag atc ccg tgt gaa gaa aag	1086		
109	Pro Asn Glu Ser Ser Ala Lys Glu Pro Glu Ile Arg Cys Glu Glu Lys			
110	295 300 305 310			
112	cca gaa gac tta tta gaa gag cca cag agc atg tcg aat gaa gct cgt	1134		
113	Pro Glu Asp Leu Leu Glu Glu Pro Gln Ser Met Ser Asn Glu Ala Arg			
114	315 320 325			
116	gaa gac tct cca gac gtg acc cct cct ccc cac act ccc aga gct aga	1182		
117	Glu Asp Ser Pro Asp Val Thr Pro Pro Pro His Thr Pro Arg Ala Arg			
118	330 335 340			
120	gag gag gcc aac ggt gat gta ctt gag aca ttt atg ttt ccg tgt cag	1230		
121	Glu Glu Ala Asn Gly Asp Val Leu Glu Thr Phe Met Phe Pro Cys Gln			
122	345 350 355			
124	cac tgt gaa aga aaa ttt gca acg aag cag ggg cta gag cgt cac atg	1278		
125	His Cys Glu Arg Lys Phe Ala Thr Lys Gln Gly Leu Glu Arg His Met			
126	360 365 370			
128	cac atc cac att tct acc atc aat cat got ttc aag tgc aag tac tgt	1326		
129	His Ile His Ile Ser Thr Ile Asn His Ala Phe Lys Cys Lys Tyr Cys			
130	375 380 385 390			

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132 ggg aaa cgg ttt ggc aca cag att aac agg agg cgg cat gaa cgg cgc 1374
133 Gly Lys Arg Phe Gly Thr Gln Ile Asn Arg Arg Arg His Glu Arg Arg
134          395          400          405
136 cac gaa acg ggg ttg aag aga aga ccc agc atg act tta cag tcc tca 1422
137 His Glu Thr Gly Leu Lys Arg Arg Pro Ser Met Thr Leu Gln Ser Ser
138          410          415          420
140 gag gat cca gat gat ggc aag ggg gaa aat gtt act tct aaa gat gag 1470
141 Glu Asp Pro Asp Asp Gly Lys Gly Glu Asn Val Thr Ser Lys Asp Glu
142          425          430          435
144 tca agt cca cct caa ctc ggg caa gac tgt ttg ata ttg aac tca gag 1518
145 Ser Ser Pro Pro Gln Leu Gly Gln Asp Cys Leu Ile Leu Asn Ser Glu
146          440          445          450
148 aaa acc tca cag gaa gta ctg aat tca tct ttt gtg gaa gaa aat ggt 1566
149 Lys Thr Ser Gln Glu Val Leu Asn Ser Ser Phe Val Glu Glu Asn Gly
150 455          460          465          470
152 gaa gtt aaa gaa ctt cat ccg tgc aaa tac tgc aaa aag gta ttt gga 1614
153 Glu Val Lys Glu Leu His Pro Cys Lys Tyr Cys Lys Lys Val Phe Gly
154          475          480          485
156 act cac acc aat atg aga cga cat cag cgt aga gtt cat gag cgc cac 1662
157 Thr His Thr Asn Met Arg Arg His Gln Arg Arg Val His Glu Arg His
158          490          495          500
160 ctg att ccc aaa ggt gtc agg cga aaa gga gga ctt ctg gaa gag cca 1710
161 Leu Ile Pro Lys Gly Val Arg Arg Lys Gly Gly Leu Leu Glu Glu Pro
162          505          510          515
164 cag cca cca gca gag cag gct cca ccc tcc cag aat gtc tat gtc cca 1758
165 Gln Pro Pro Ala Glu Gln Ala Pro Pro Ser Gln Asn Val Tyr Val Pro
166          520          525          530
168 agc aca gag cca gag gag gaa ggg gaa aca gat gac gtg tac atc atg 1806
169 Ser Thr Glu Pro Glu Glu Glu Gly Glu Thr Asp Asp Val Tyr Ile Met
170 535          540          545          550
172 gac att tct agc aac atc tct gaa aac cta aat tac tat att gac ggt 1854
173 Asp Ile Ser Ser Asn Ile Ser Glu Asn Leu Asn Tyr Tyr Ile Asp Gly
174          555          560          565
176 aag att cag acc aac agc agc act agt aac tgt gat gtg att gag atg 1902
177 Lys Ile Gln Thr Asn Ser Ser Thr Ser Asn Cys Asp Val Ile Glu Met
178          570          575          580
180 gag tct aat tct gca cac ttg tat ggc ata gac tgt ctg ctc act cca 1950
181 Glu Ser Asn Ser Ala His Leu Tyr Gly Ile Asp Cys Leu Leu Thr Pro
182          585          590          595
184 gtg acc gtg gag att act cag aac ata aag agc act cag gtc tct gtg 1998
185 Val Thr Val Glu Ile Thr Gln Asn Ile Lys Ser Thr Gln Val Ser Val
186          600          605          610
188 aca gat gat ctt ctc aaa gac tct ccc agc agc aca aat tgt gag tct 2046
189 Thr Asp Asp Leu Leu Lys Asp Ser Pro Ser Ser Thr Asn Cys Glu Ser
190 615          620          625          630
192 aag aaa cgg agg act gcc agt cca cct gtg ctc ccc aaa att aaa acg 2094
193 Lys Lys Arg Arg Thr Ala Ser Pro Pro Val Leu Pro Lys Ile Lys Thr
194          635          640          645
196 gag acg gag tct gat tcc aca gca ccc tcg tgt tcc tta agt ctg ccc 2142

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197	Glu	Thr	Glu	Ser	Asp	Ser	Thr	Ala	Pro	Ser	Cys	Ser	Leu	Ser	Leu	Pro	
198				650					655					660			
200	ctg	agc	ata	tcc	aca	gcc	gag	gtg	gtg	tcc	ttc	cat	aaa	gag	aag	ggc	2190
201	Leu	Ser	Ile	Ser	Thr	Ala	Glu	Val	Val	Ser	Phe	His	Lys	Glu	Lys	Gly	
202				665					670					675			
204	gtc	tat	ttg	tcg	tcc	aag	ctc	aag	cag	ctt	ctt	cag	acc	cag	gac	aag	2238
205	Val	Tyr	Leu	Ser	Ser	Lys	Leu	Lys	Gln	Leu	Leu	Gln	Thr	Gln	Asp	Lys	
206				680					685					690			
208	ctg	acc	ctt	cct	gca	ggg	ttt	tca	gca	gct	gag	att	cct	aag	tta	ggt	2286
209	Leu	Thr	Leu	Pro	Ala	Gly	Phe	Ser	Ala	Ala	Glu	Ile	Pro	Lys	Leu	Gly	
210	695					700					705					710	
212	ccc	gtg	tgc	gcg	tct	gct	cct	gca	tcc	atg	ttg	ccc	gtg	acc	tct	agt	2334
213	Pro	Val	Cys	Ala	Ser	Ala	Pro	Ala	Ser	Met	Leu	Pro	Val	Thr	Ser	Ser	
214					715					720						725	
216	agg	ttt	aag	aga	cgc	acc	agc	tct	cca	ccg	agc	tct	cca	cag	cac	agc	2382
217	Arg	Phe	Lys	Arg	Arg	Thr	Ser	Ser	Pro	Pro	Ser	Ser	Pro	Gln	His	Ser	
218					730					735						740	
220	cct	gcc	ctt	cga	gac	ttc	ggg	aaa	cca	aat	gat	ggg	aaa	gca	gca	tgg	2430
221	Pro	Ala	Leu	Arg	Asp	Phe	Gly	Lys	Pro	Asn	Asp	Gly	Lys	Ala	Ala	Trp	
222				745					750					755			
224	aca	gac	aca	gtc	ctg	act	tcc	aag	aaa	ccc	aag	tta	gaa	agt	cgt	agt	2478
225	Thr	Asp	Thr	Val	Leu	Thr	Ser	Lys	Lys	Pro	Lys	Leu	Glu	Ser	Arg	Ser	
226				760					765					770			
228	gac	tca	cca	gca	tgg	agt	ttg	tct	ggg	aga	gat	gaa	aga	gaa	acc	gga	2526
229	Asp	Ser	Pro	Ala	Trp	Ser	Leu	Ser	Gly	Arg	Asp	Glu	Arg	Glu	Thr	Gly	
230	775					780					785					790	
232	agc	cct	cct	tgc	ttt	gat	gaa	tac	aaa	ata	tca	aag	gaa	tgg	gca	gcc	2574
233	Ser	Pro	Pro	Cys	Phe	Asp	Glu	Tyr	Lys	Ile	Ser	Lys	Glu	Trp	Ala	Ala	
234					795					800						805	
236	agt	tct	act	ttc	agc	agt	gtg	tgc	aac	caa	cag	cca	ttg	gat	tta	tcc	2622
237	Ser	Ser	Thr	Phe	Ser	Ser	Val	Cys	Asn	Gln	Gln	Pro	Leu	Asp	Leu	Ser	
238				810					815							820	
240	agc	ggg	gtc	aaa	cag	aag	tca	gag	ggc	aca	ggc	aag	act	cca	gtc	cca	2670
241	Ser	Gly	Val	Lys	Gln	Lys	Ser	Glu	Gly	Thr	Gly	Lys	Thr	Pro	Val	Pro	
242				825					830					835			
244	tgg	gaa	tct	gta	ttg	gat	ctc	agt	gtg	cat	aaa	aag	cct	tgc	gat	tct	2718
245	Trp	Glu	Ser	Val	Leu	Asp	Leu	Ser	Val	His	Lys	Lys	Pro	Cys	Asp	Ser	
246				840					845					850			
248	gaa	ggc	aag	gaa	ttc	aaa	gag	aac	cat	ttg	gca	cag	cca	gct	gca	aag	2766
249	Glu	Gly	Lys	Glu	Phe	Lys	Glu	Asn	His	Leu	Ala	Gln	Pro	Ala	Ala	Lys	
250	855					860					865					870	
252	aag	aaa	aaa	cca	acc	acc	tgt	atg	ctt	caa	aag	gtt	ctt	ctc	aat	gag	2814
253	Lys	Lys	Lys	Pro	Thr	Thr	Cys	Met	Leu	Gln	Lys	Val	Leu	Leu	Asn	Glu	
254					875					880						885	
256	tat	aat	ggt	gtt	agc	tta	cct	aca	gaa	acc	aca	cca	gag	gtg	acc	agg	2862
257	Tyr	Asn	Gly	Val	Ser	Leu	Pro	Thr	Glu	Thr	Thr	Pro	Glu	Val	Thr	Arg	
258				890					895					900			
260	agc	cca	agt	cct	tgt	aaa	tcc	cca	gat	aca	cag	cca	gat	cct	gaa	ctt	2910
261	Ser	Pro	Ser	Pro	Cys	Lys	Ser	Pro	Asp	Thr	Gln	Pro	Asp	Pro	Glu	Leu	

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262	905	910	915	
264	ggt cct gac tca agt tgc tca gtc ccc act gct gag tct cca cct gaa	2958		
265	Gly Pro Asp Ser Ser Cys Ser Val Pro Thr Ala Glu Ser Pro Pro Glu			
266	920 925 930			
268	ggt ggt ggc cct tcc tca ccc cct ctc cag aca gcc tcc tta tcc tcc	3006		
269	Val Val Gly Pro Ser Ser Pro Pro Leu Gln Thr Ala Ser Leu Ser Ser			
270	935 940 945 950			
272	ggt cag ctg cct cct ctc tta acc ccc aca gag cct tct tcc cct ccc	3054		
273	Gly Gln Leu Pro Pro Leu Leu Thr Pro Thr Glu Pro Ser Ser Pro Pro			
274	955 960 965			
276	ccc tgc cct cct gtg tta act gtt gcc act cca cca cct ccc ctc ctt	3102		
277	Pro Cys Pro Pro Val Leu Thr Val Ala Thr Pro Pro Pro Pro Leu Leu			
278	970 975 980			
280	cca acc gtc cct ctc tcc cac ccc tct tct gat gcc tcc cct cag cag	3150		
281	Pro Thr Val Pro Leu Ser His Pro Ser Ser Asp Ala Ser Pro Gln Gln			
282	985 990 995			
284	tgt ccc tct ccg ttc tca aac acc act gct cag tct cct ctt ccc att	3198		
285	Cys Pro Ser Pro Phe Ser Asn Thr Thr Ala Gln Ser Pro Leu Pro Ile			
286	1000 1005 1010			
288	ctc tcc cca aca gtg tct ccc tct ccc tct ccc att cct cct gta gag	3246		
289	Leu Ser Pro Thr Val Ser Pro Ser Pro Ser Pro Ile Pro Pro Val Glu			
290	1015 1020 1025 1030			
292	cca ctt atg tct gct gct tcc cct ggt ccc cca aca ctt tct tcc tcc	3294		
293	Pro Leu Met Ser Ala Ala Ser Pro Gly Pro Pro Thr Leu Ser Ser Ser			
294	1035 1040 1045			
296	tcc tct tct tcc tct tcc ttc cct tcc tct tcc tgc tcc tcc acc tcc	3342		
297	Ser Ser Ser Ser Ser Ser Phe Pro Ser Ser Ser Cys Ser Ser Thr Ser			
298	1050 1055 1060			
300	ccc tcc cca ccc cct ctt tca gca gtg tca tct gtg gtt tcc tct ggg	3390		
301	Pro Ser Pro Pro Pro Leu Ser Ala Val Ser Ser Val Val Ser Ser Gly			
302	1065 1070 1075			
304	gac aac ctg gag gca tct ctg cct gca gta act ttc aaa cag gag gag	3438		
305	Asp Asn Leu Glu Ala Ser Leu Pro Ala Val Thr Phe Lys Gln Glu Glu			
306	1080 1085 1090			
308	tca gag agt gaa ggt ctg aaa ccc aag gaa gag gcc cca cct gca ggg	3486		
309	Ser Glu Ser Glu Gly Leu Lys Pro Lys Glu Glu Ala Pro Pro Ala Gly			
310	1095 1100 1105 1110			
312	gga cag agt gtg gtc caa gaa aca ttc agc aaa aac ttc att tgc aat	3534		
313	Gly Gln Ser Val Val Gln Glu Thr Phe Ser Lys Asn Phe Ile Cys Asn			
314	1115 1120 1125			
316	gtc tgt gaa tcg cct ttt ctt tcc att aaa gac cta acc aaa cat tta	3582		
317	Val Cys Glu Ser Pro Phe Leu Ser Ile Lys Asp Leu Thr Lys His Leu			
318	1130 1135 1140			
320	tcc gtc cat gct gaa gag tgg ccc ttc aaa tgt gag ttt tgt gtg cag	3630		
321	Ser Val His Ala Glu Glu Trp Pro Phe Lys Cys Glu Phe Cys Val Gln			
322	1145 1150 1155			
324	ctg ttt aag gtt aag act gat cta tca gag cat cga ttt ctg ctt cat	3678		
325	Leu Phe Lys Val Lys Thr Asp Leu Ser Glu His Arg Phe Leu Leu His			
326	1160 1165 1170			

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date